



1/29

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTGCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGGAGCGGCCGCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCGCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAAGTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

Fig. 1

TECH CENTER 1600/2900

APR 24 2003

RECEIVED



3/29

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query: 289 TACCGAAGAGGCTGTGGTCTGCGGGTGCCCTGCACGCTGCCGTGCGGCAGGATCTGCA 230
      |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTGCGGGTGCCCTGCACGCTGCCGTGCGGCAGGATCTGCA 15986

Query: 229 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
      |||
Sbjct: 15987 GGTGGAAGCCGGTGCGGCAATAGAGCTGCCGGCG-CGAGGATGCCGTGCAGGTGCGCCA 16045

Query: 169 GCTGCGCAGCCCCGCGCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 110
      |||
Sbjct: 16046 GCTGCGCAGCCCCGCGCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 16105

Query: 109 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
      |||
Sbjct: 16106 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query: 49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
      |||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query: 633 AGTGTACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 574
      |||
Sbjct: 7257 AGTGTACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 7316

Query: 573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCGGTC 514
      |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCGGTC 7376

Query: 513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
      |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query: 453 ATAGGTGTTATACCAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 394
      |||
Sbjct: 7437 ATAGGTGTTATACCAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 7496
```

Fig.3

RECEIVED
APR 24 2003
GEN CENTER 1600/2900



QUERY: 393 CTC-TGATCCATAGA 380
 ||| ||| | |||
Sbjct: 7497 CTCCTGAAAGAGAGA 7511

C.
Score = 530 (75.9 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 106/106 (100%), Positives = 106/106 (100%),
Strand = Minus / Plus

QUERY: 391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
 |||||
Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

QUERY: 331 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 286
 |||||
Sbjct: 9897 TAATACTGACCAGTCCCCTGCCCACACTGATGAATTCCAAGATACC 9942

Fig.3
(CONTINUED)

RECEIVED
APR 24 2003
TECH CENTER 1500/2900



Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9	MAPLGEVGN ¹⁰ YFGVQDAVP--FGNV ¹⁰ VPVLP--VDS ¹⁰ PVLLSDHLGQSEAGGLPRGPAVTDLDH
RAT FGF-9	MAPLGEVGS ¹⁰ YFGVQDAVP--FGNV ¹⁰ VPVLP--VDS ¹⁰ PVLLSDHLGQSEAGGLPRGPAVTDLDH
MOUSE FGF-9	MAPLGEVGS ¹⁰ YFGVQDAVP--FGNV ¹⁰ VPVLP--VDS ¹⁰ PVLLNDHLGQSEAGGLPRGPAVTDLDH
XENOPUS XFGF-CX	MAPLAD ¹⁰ VGCH ¹⁰ FLGGYDAN ¹⁰ G-QVGS ¹⁰ HF ¹⁰ LP ¹⁰ PAK ¹⁰ DS ¹⁰ PLFND ¹⁰ PL ¹⁰ QSERLSR-SAP--SDLSH
FGF-CX	MAPLAEVGGELGGL ¹⁰ EG ¹⁰ LG ¹⁰ GGQVGS ¹⁰ HF ¹⁰ LP ¹⁰ PAGE ¹⁰ RP ¹⁰ PL ¹⁰ GER ¹⁰ RSAAERSAR-GGPF ¹⁰ GA ¹⁰ Q ¹⁰ LAH
HUMAN FGF-9	LKGILRRRQLYCR ¹⁰ TGFHLEIFP ¹⁰ NGTIQ ¹⁰ TRK ¹⁰ DHS ¹⁰ RF ¹⁰ GILEFISIAVGLVSIRGVDSGLYL
RAT FGF-9	LKGILRRRQLYCR ¹⁰ TGFHLEIFP ¹⁰ NGTIQ ¹⁰ TRK ¹⁰ DHS ¹⁰ RF ¹⁰ GILEFISIAVGLVSIRGVDSGLYL
MOUSE FGF-9	LKGILRRRQLYCR ¹⁰ TGFHLEIFP ¹⁰ NGTIQ ¹⁰ TRK ¹⁰ DHS ¹⁰ RF ¹⁰ GILEFISIAVGLVSIRGVDSGLYL
XENOPUS XFGF-CX	LQ ¹⁰ GILRRRQLYCR ¹⁰ TGFHL ¹⁰ Q ¹⁰ IL ¹⁰ PD ¹⁰ GN ¹⁰ Q ¹⁰ Q ¹⁰ TR ¹⁰ Q ¹⁰ DHS ¹⁰ RF ¹⁰ GILEFISIA ¹⁰ VGLVSIRGVDT ¹⁰ GLYL
FGF-CX	LHGILRRRQLYCR ¹⁰ TGFH ¹⁰ LQ ¹⁰ IL ¹⁰ PD ¹⁰ GS ¹⁰ VQ ¹⁰ TR ¹⁰ Q ¹⁰ DHS ¹⁰ LF ¹⁰ GILEFISIAVGLVSIRGVDSGLYL
HUMAN FGF-9	GMNEKGELYGSEKLTQECV ¹⁰ FREQ ¹⁰ FEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
RAT FGF-9	GMNEKGELYGSEKLTQECV ¹⁰ FREQ ¹⁰ FEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
MOUSE FGF-9	GMNEKGELYGSEKLTQECV ¹⁰ FREQ ¹⁰ FEENWYNTYSSNLYKHVDTGRRYYVALNKDGT ¹⁰ PREGT
XENOPUS XFGF-CX	GMND ¹⁰ KGEL ¹⁰ FGSEKLT ¹⁰ SEC ¹⁰ FREQ ¹⁰ FEENWYNTYSSNLYKHG ¹⁰ DS ¹⁰ GRRY ¹⁰ FVALNKDGT ¹⁰ PRDGT
FGF-CX	GMND ¹⁰ KGELYGSEKLT ¹⁰ SEC ¹⁰ FREQ ¹⁰ FEENWYNTYSSNLYKHG ¹⁰ DTGRRY ¹⁰ FVALNKDGT ¹⁰ PRDGA
HUMAN FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPKVP ¹⁰ ELYKD ¹⁰ ILSQS
RAT FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPKVP ¹⁰ ELYKD ¹⁰ ILSQS
MOUSE FGF-9	RTKR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ DPKVP ¹⁰ ELYKD ¹⁰ ILSQS
XENOPUS XFGF-CX	RA ¹⁰ KR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ PE ¹⁰ KVP ¹⁰ ELYKD ¹⁰ EMGY ¹⁰ S
FGF-CX	RS ¹⁰ KR ¹⁰ HQKFT ¹⁰ HLPRPVD ¹⁰ PER ¹⁰ VP ¹⁰ ELYKD ¹⁰ ELMY ¹⁰ LS

Fig. 4



RECEIVED
APR 24 2003
TECH CENTER 160012900

Fig. 5



7/29

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9)
(FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208
(81%)

Query: 1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH 59
| | | | | | | + | + + | + + | | + | | + + | | |
Sbjct: 1 MAPLGEVGNFYGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query: 60 LHGILPRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGLVSIRGVDSGLYL 119
| | | | | | | | | | | | | | + | + | + | | | | | | | + | | | | | | | | | | | |
Sbjct: 57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query: 120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
| | | + | | | | | | | | | + | | | | | | | | | + | | | | | + | | | | | + | |
Sbjct: 117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query: 180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
| + | | | | | | | | | | | | | + + | | | | | + |
Sbjct: 177 RTRRHQKFTHFLPRPVDPKVPELYKDIL 205

Fig. 6

RECEIVED
APR 24 2003
TECH CENTER 1600/2900



LENGTH = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
          ||||| ||| + | + + | + + || + | || + + | || ||
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFGILEFISVAVGLVSIRGVDSGLYL 119
          | ||||| ||||| ||||| + | + | ++ ||| + ||| ||||| ||||| + ||||| ||||| |||||
Sbjct:     57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:    120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
          ||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||| ||||| ||||| + |||
Sbjct:    117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:    180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
          | + ||||| ||||| ||||| ++ ||||| ||| + |
Sbjct:    177 RTKRHQKFTHFLPRPVDPKVPELYKDIL 205
```

Fig. 7



9/29

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```
Query:   1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
          ||||| ||| + | + + | + + || + || + + | ||
Sbjct:   1 MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH 56

Query:  60 LHGILRRRQLYCRTGFHLQILPDGSVQGTQDHSLEFGILEFISVAVGLVSIRGVDSGLYL 119
          | ||||| ||||| ||||| + | + | ++ ||| + ||| ||||| ||||| + ||||| |||||
Sbjct:  57 LKGILRRRQLYCRTGFHLEIFPNGTIQGTQDHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query: 120 GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
          ||| + ||||| ||||| ||| + ||||| ||||| ||||| + ||||| ||||| + |||||
Sbjct: 117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query: 180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
          | + ||||| ||||| ||||| ++ ||||| ||| + |
Sbjct: 177 RTKRHQKFTHFLPRPVDPDKVPELYKDIL 205
```

Fig. 8

RECEIVED
APR 24 2003
TECH CENTER 1600/2900



10/29

FGF-CX Query Length = 211
XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P= 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

```
Query:    1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL 60
          |||||+|| |||| + ||| ||||| ||||| ||||| + | | + + + || + | | + |||
Sbjct:    1 MAPLADVGTFLGGYDALGQ-VGSFLLPPAKDSPLL FNDPLAQSERLSRSAP--SDLSHL 57

Query:    61 HGILRRRQLYCRTGFHLQILPDGQVQTRQDHSFGILEFISVAVGLVSIRGVDSGLYL 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    58 QGILRRRQLYCRTGFHLQILPDGNVQTRQDHSRFGILEFISVAIGLVSIRGVDTGLYL 117

Query:    121 MNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRD 180
          ||||| + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    118 MNDKGELFGSEKLTSECFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRD 177

Query:    181 SKRHQKFTHFLPRPVDPERVPELYKDLLMYT 211
          + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    178 AKRHQKFTHFLPRPVDPEKVPPELYKDLMGYS 208
```

Fig. 9

RECEIVED
APR 24 2003
TECH CENTER 1600/2900



11/29

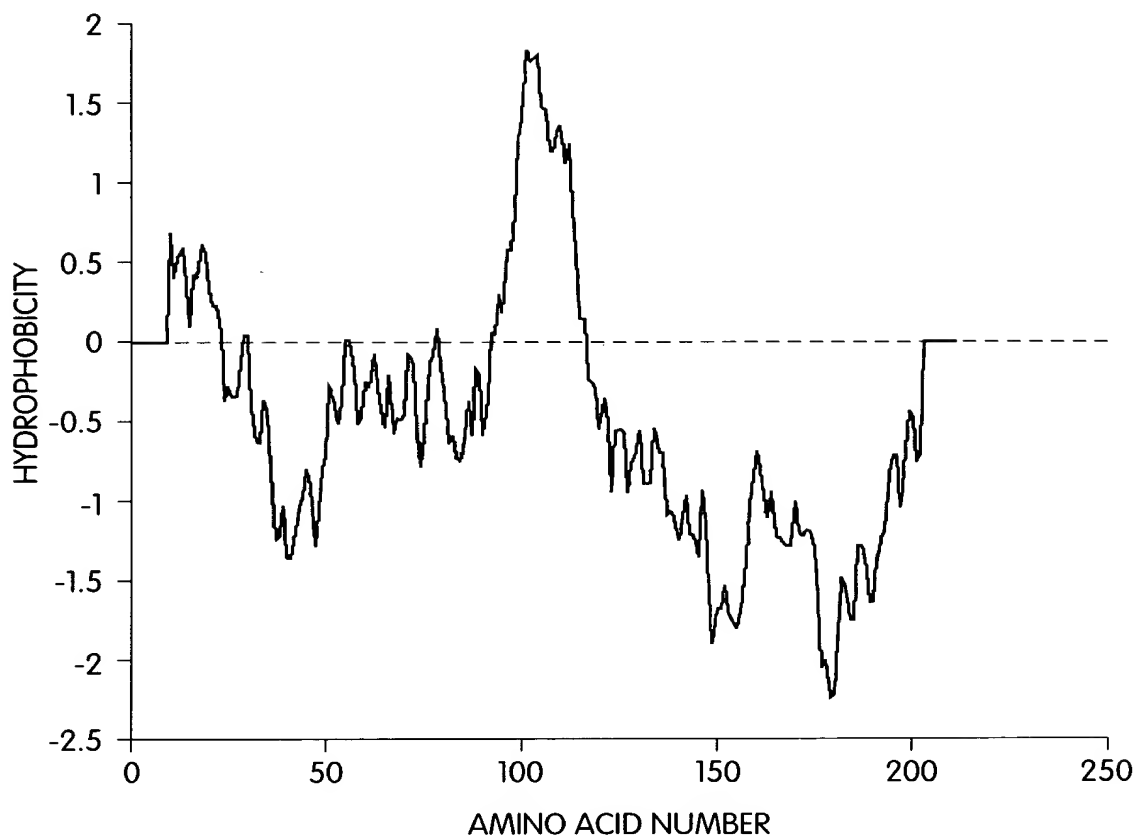


Fig. 10

RECEIVED
APR 24 2003
TECH CENTER 1600/2900



12/29

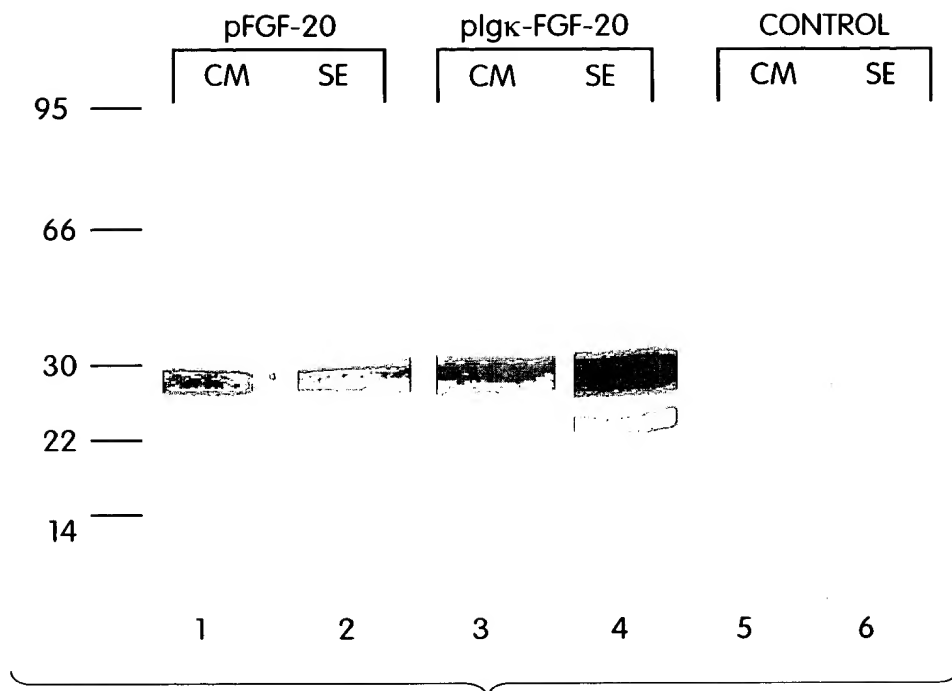


Fig. 11A

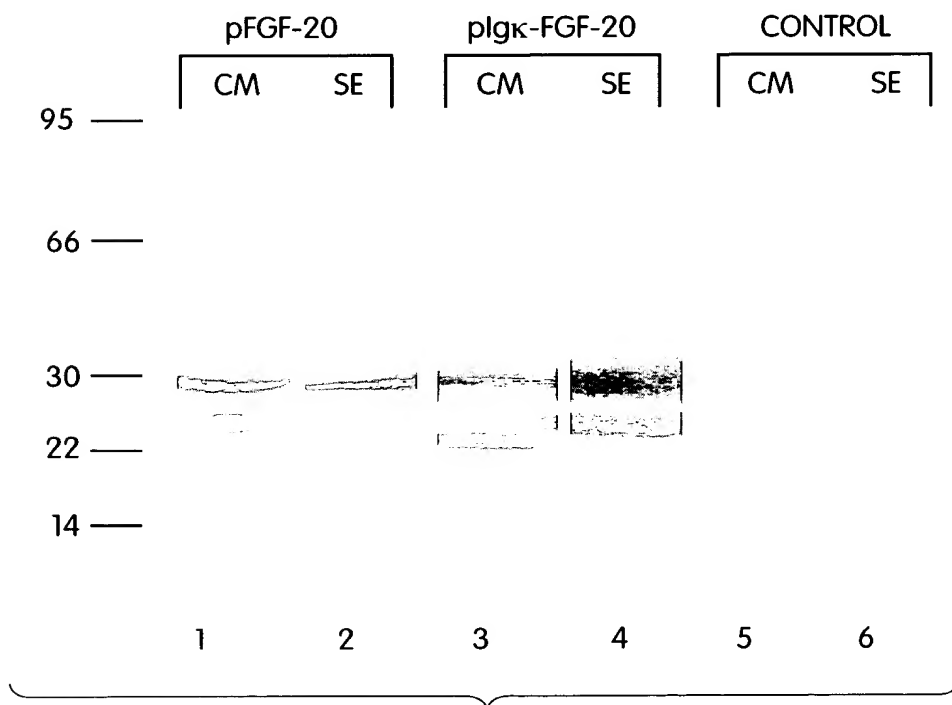


Fig. 11B

RECEIVED
APR 24 2003
TECH CENTER 10001200



13/29

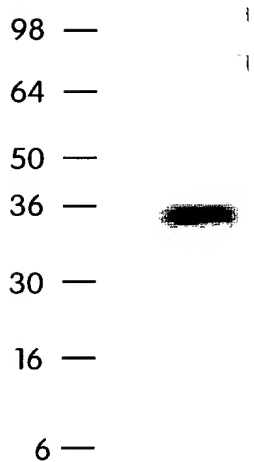


Fig. 12

RECEIVED
APR 24 2003
TECH CENTER 160012900



Exon 1

...AGACAGTGAGACTTCCCTGCCATTTCAGTGCAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGGGCCCTTAAC

TTTTGGCGCTCGTTTGGCTATAAATTTTCTCTATCCACTCCCATCCACCCCAACACTCTTTACTGGGGGGGTCTTTT

GTGTTCCGGATCTCCCCCTCCATGGCTCCCTTAGCGGAAGTCGGGGGCTTTCTGGGGGGCTGGAGGCTTGGGCCAGCA

1 M A P L A E V G G F L G G L E G L G Q Q

GGTGGGTTCCGATTTCTGTGCTCCTGCGGGGAGCGGCCCGCTGCTGGCGAGCGCAGGAGCGCGGGGAGCGGA

21 V G S H F L L P P A G E R P P L L G E R R S A A E R S

GCGCGCGCGGGGGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCTCGCGCGCGCGCAGCTTATTCGCGCAC

48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T

GGCTTCCACTGCAGATCCTGCCGACGCGAGCGTGCAGGGCACCGGAGGACACAGCCTCTTCGGTATCTTGGAAAT

<-|-> Exon 2

74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F

CATCAGTGGCAGTGGGACTGGTCAGTATTAGAGTGTGGACAGTGGTCTCTATCTTGGATGAATGACAAAGGAGAAC

101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L

<-|-> Exon 3

TCTATGGATCAGAGAACTTACTCCGAATGCATCTTAGGAGCAGTTGAAGAGAAGTGTATACACCTATTTCATCT

128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S

AACATATATAACATGGAGACACTGGCCGAGGATTTTGTGGCACTTAACAAAGACGGAATCCACAGATGGCGCCAG

154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R

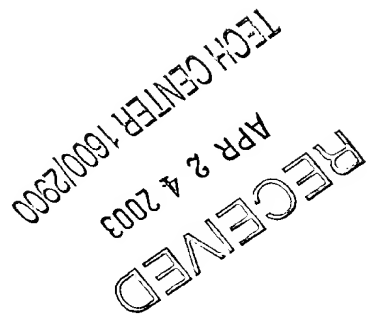
GTCCAAGAGCATCAGAAATTTACACATTTCTTACTAGACAGTGGATCCAGAAAGAGTTCCAGAAATGTACAGGACC

181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L

TACTGATGTACACTTGA...

208 L M Y T

Fig. 13





15/29

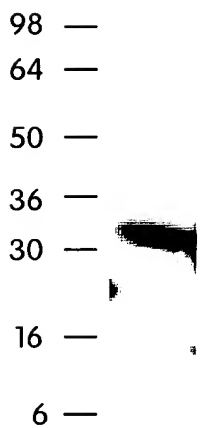


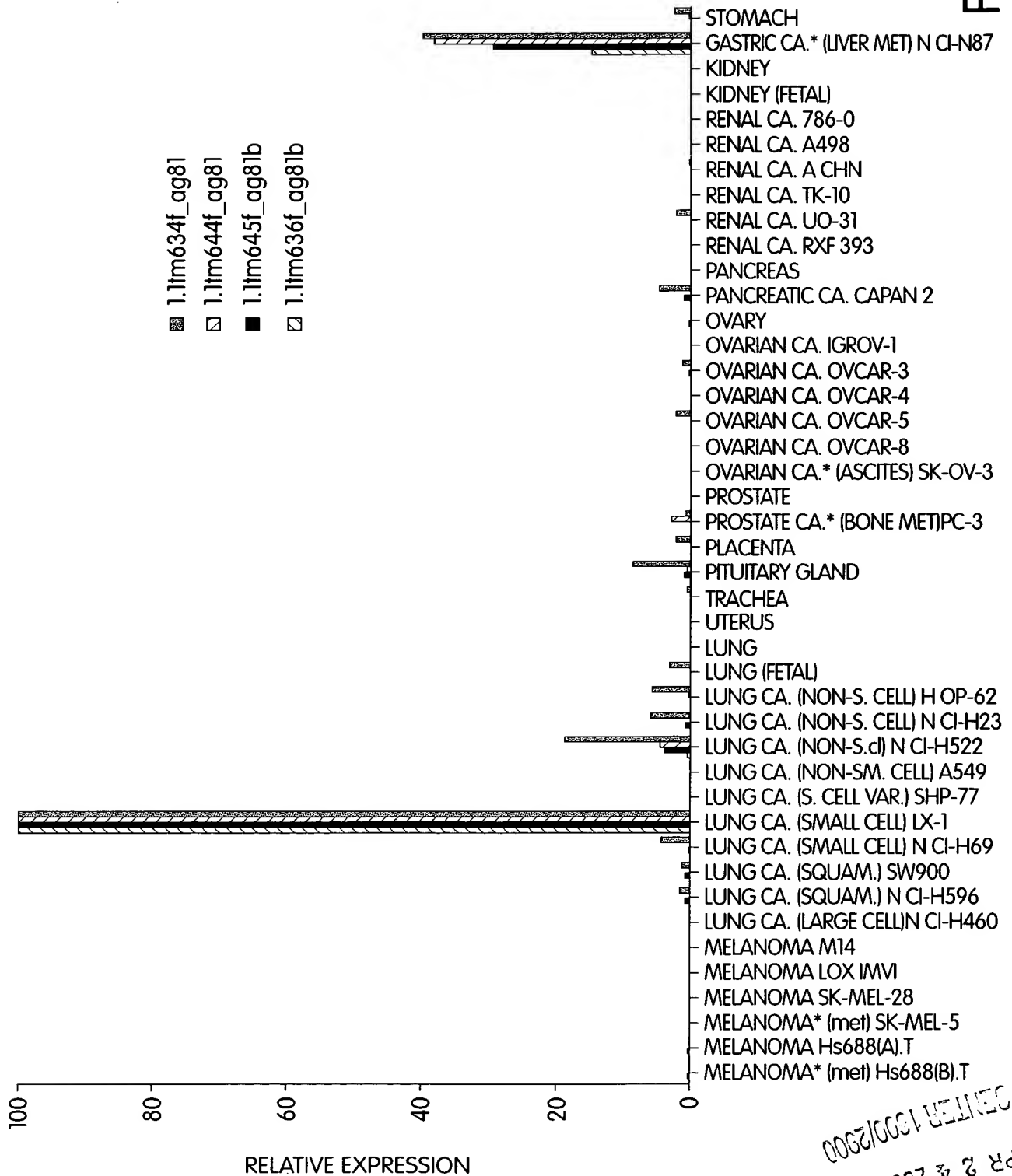
Fig. 14

RECEIVED
APR 24 2003
TECH CENTER 1600/2900
RECEIVED
APR 24 2003



16/29

Fig. 15A



RECEIVED
APR 24 2003
TECH CENTER 1509/2500



17/29

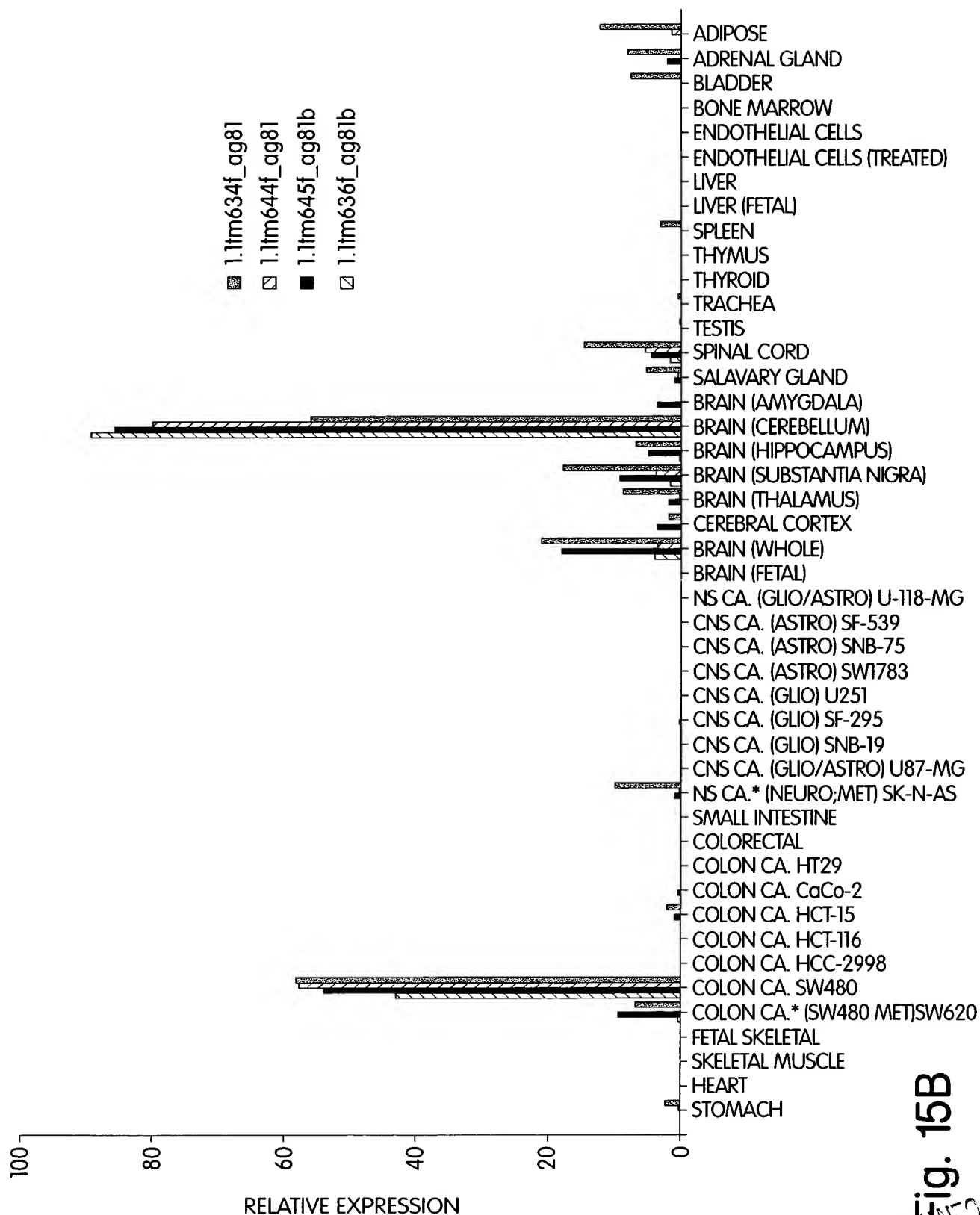


Fig. 15B

RECEIVED
APR 24 2003
TECH CENTER 1500/2900

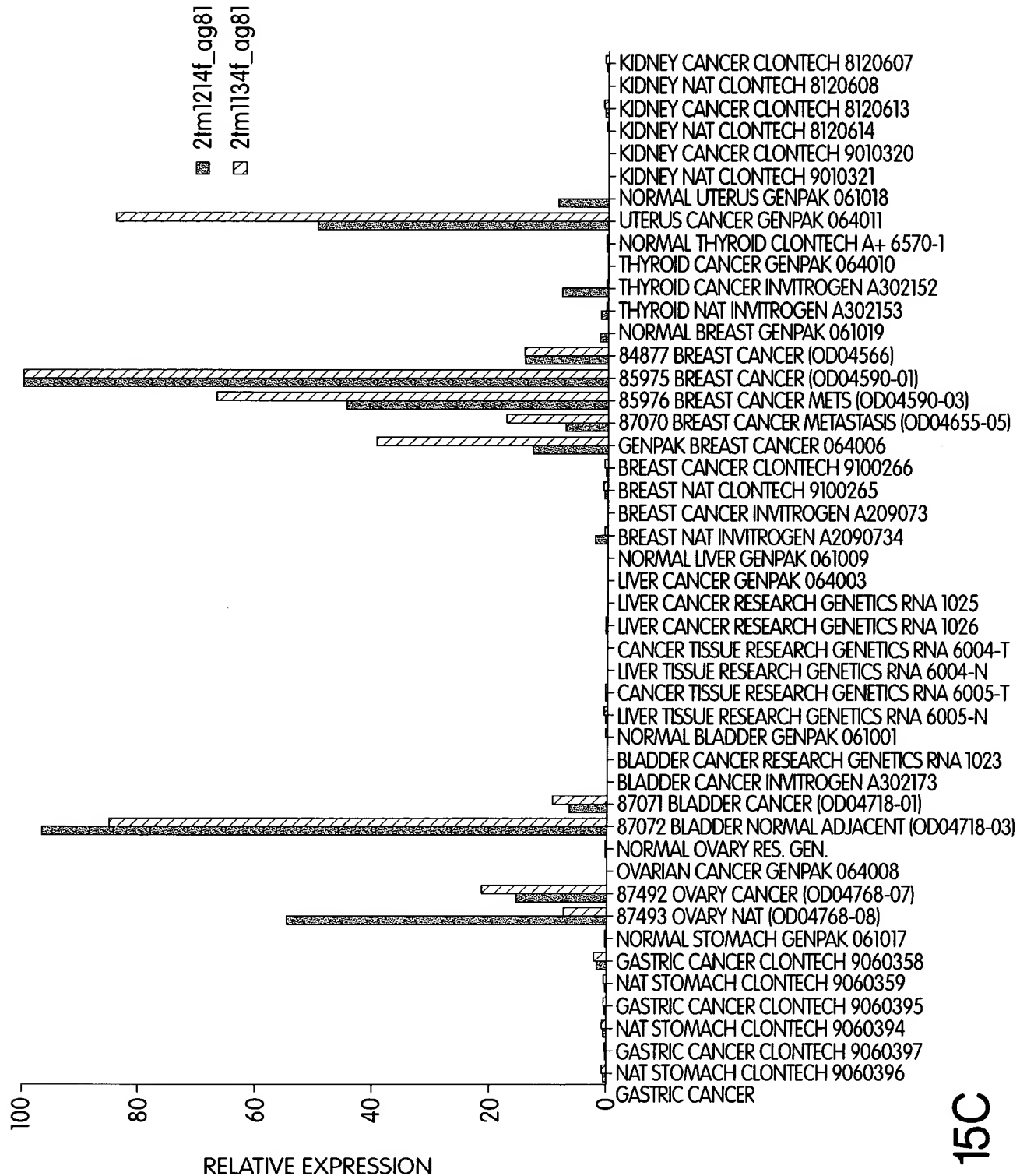
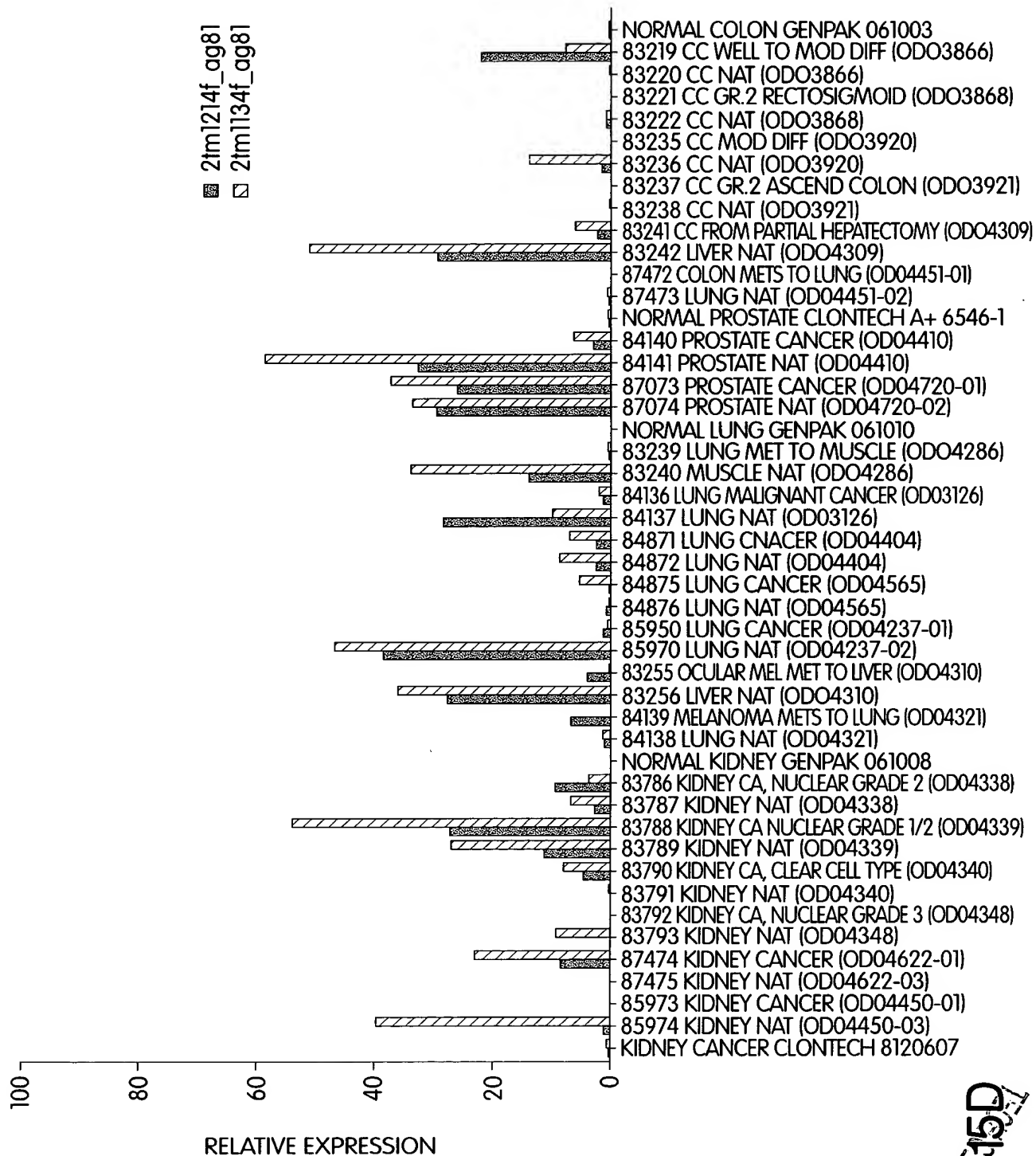


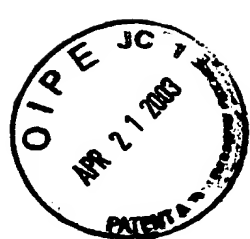
Fig. 15C



19/29



RECEIVED
APR 24 2003
Fig. 6f
1600/2900



20/29

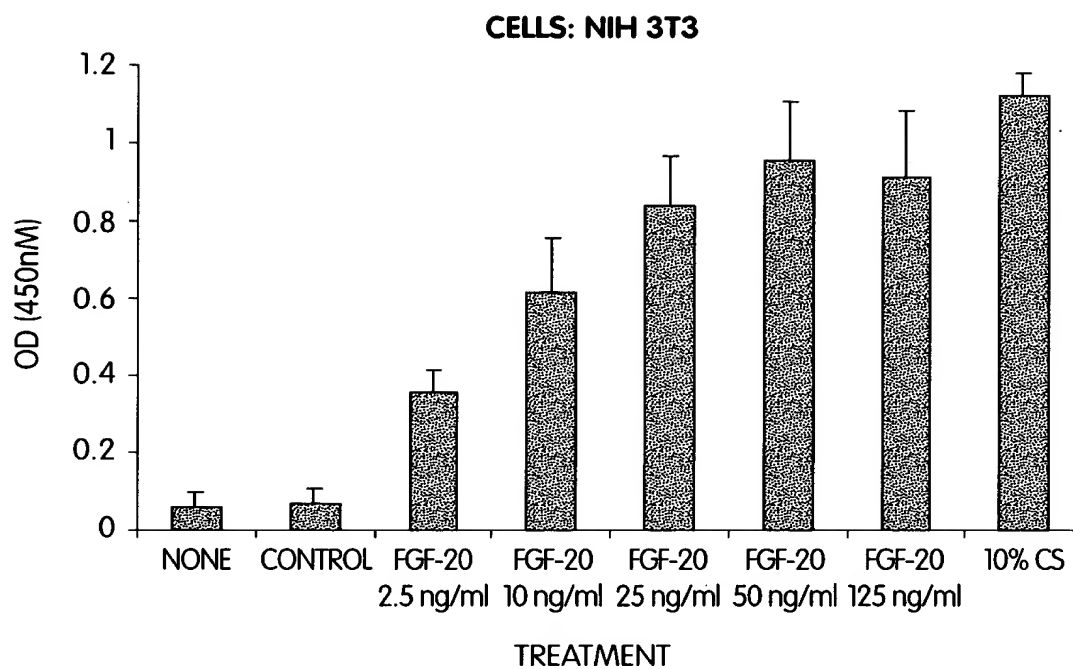


Fig. 16A

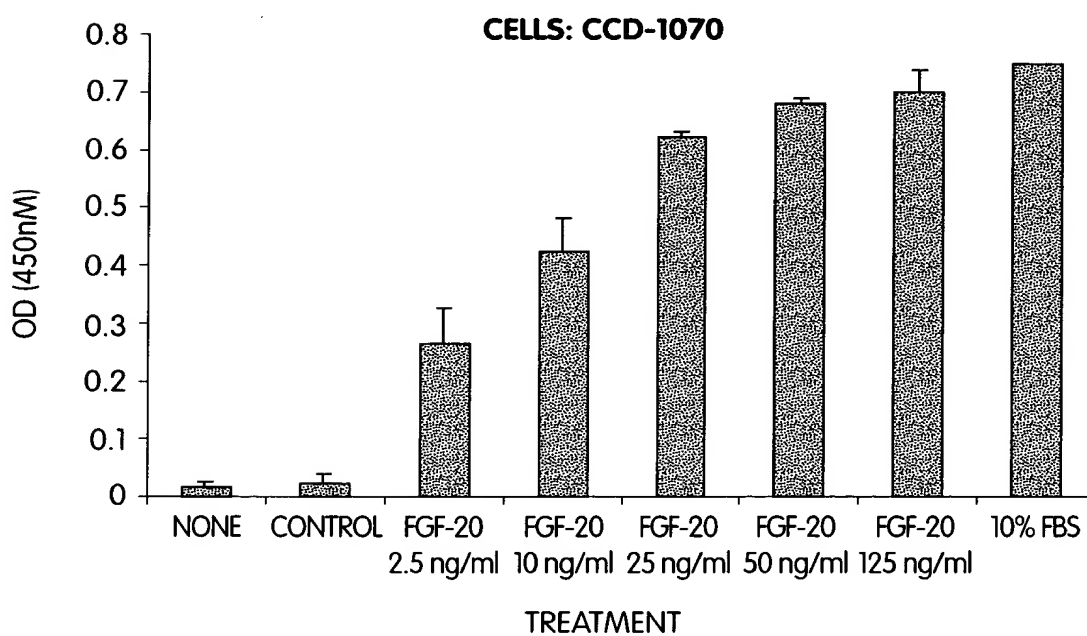
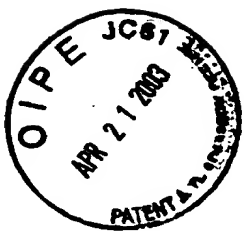


Fig. 16B

RECEIVED
APR 24 2003
TECH CENTER 1000 600



21/29

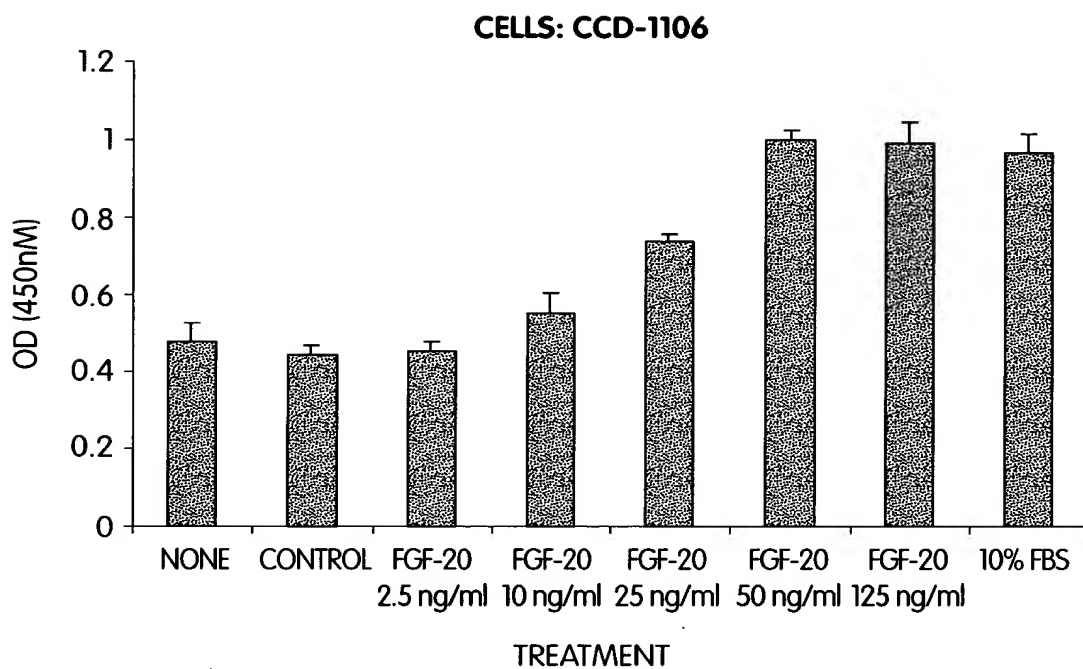


Fig. 16C

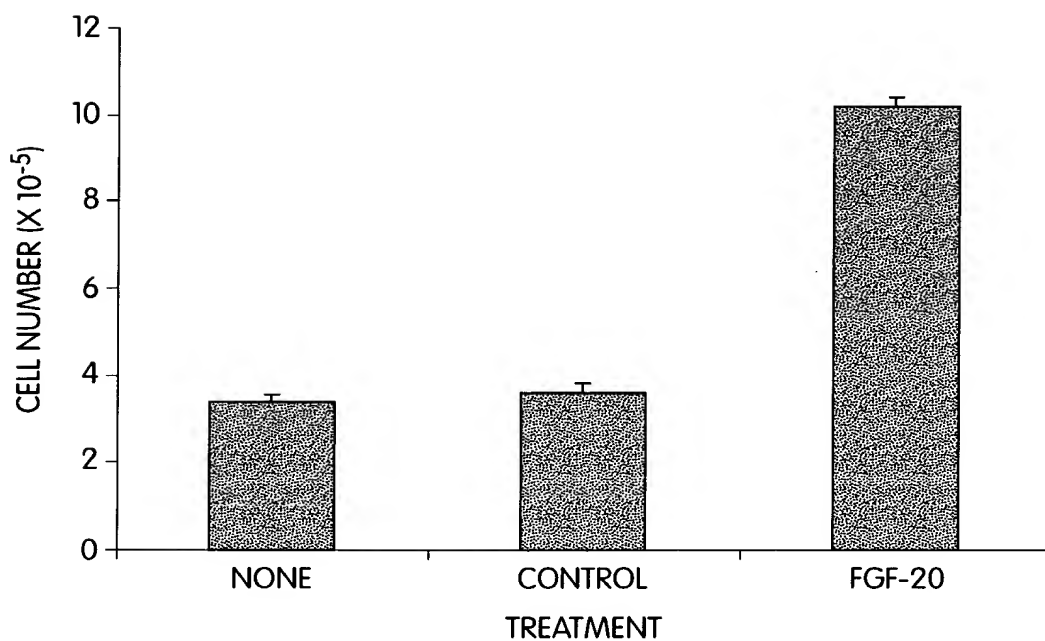


Fig. 17

RECEIVED
APR 24 2003
TECH CENTER 1600/2900

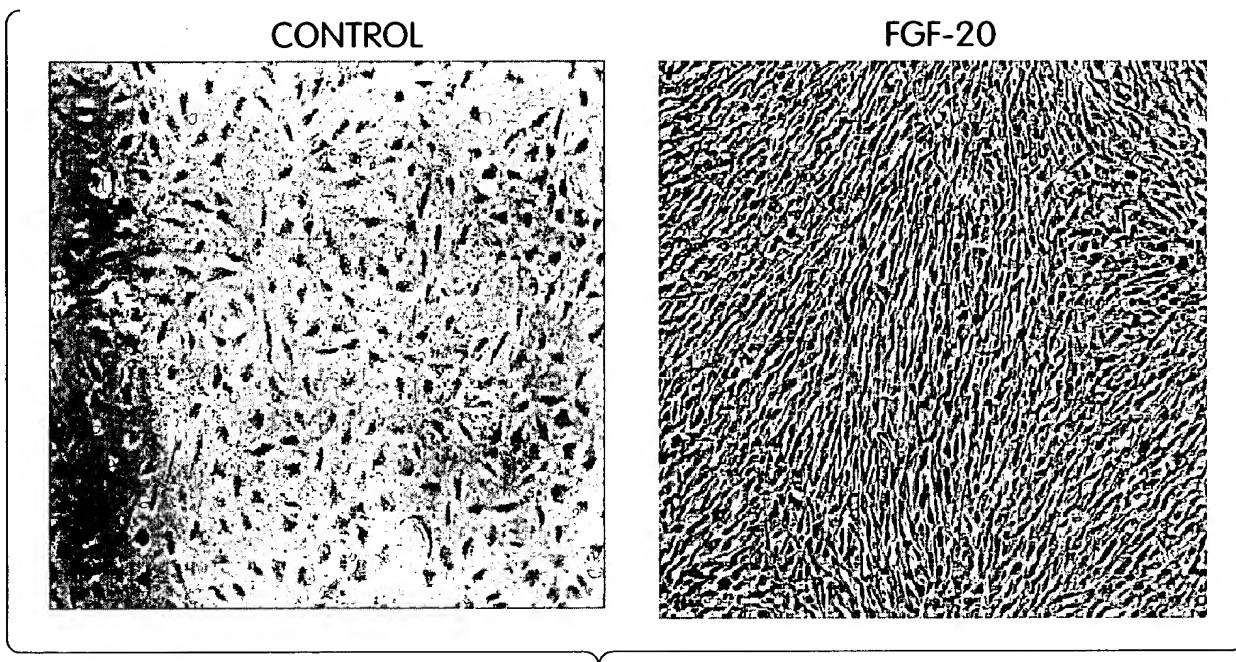


Fig. 18

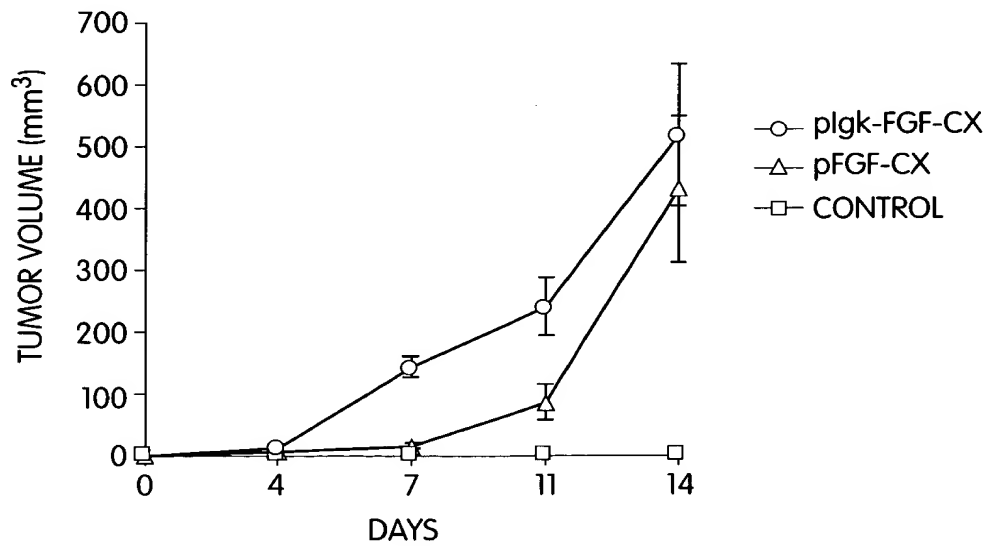
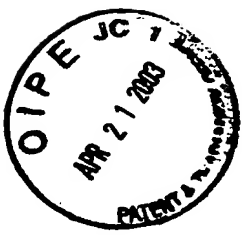


Fig. 19

RECEIVED
APR 24 2003
TECH CENTER 1000 1000



23/29

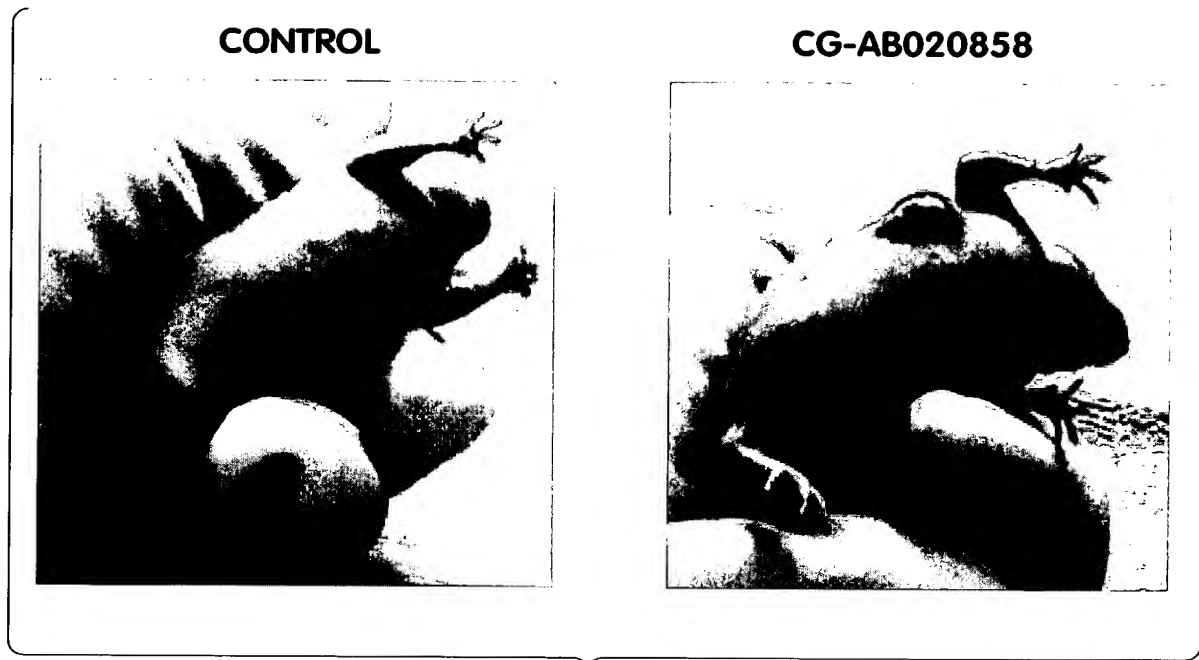


Fig. 20

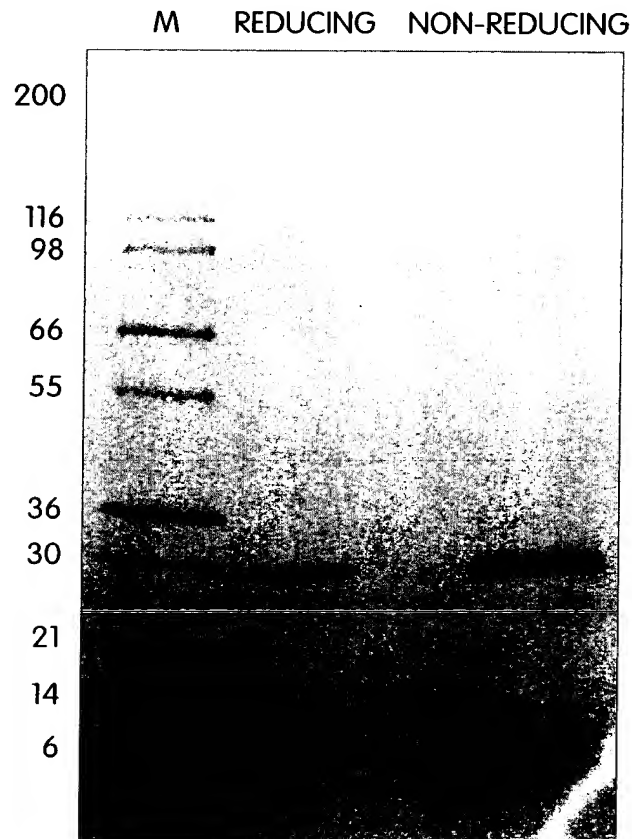


Fig. 21

RECEIVED
APR 24 2003
TECH CENTER 10012900

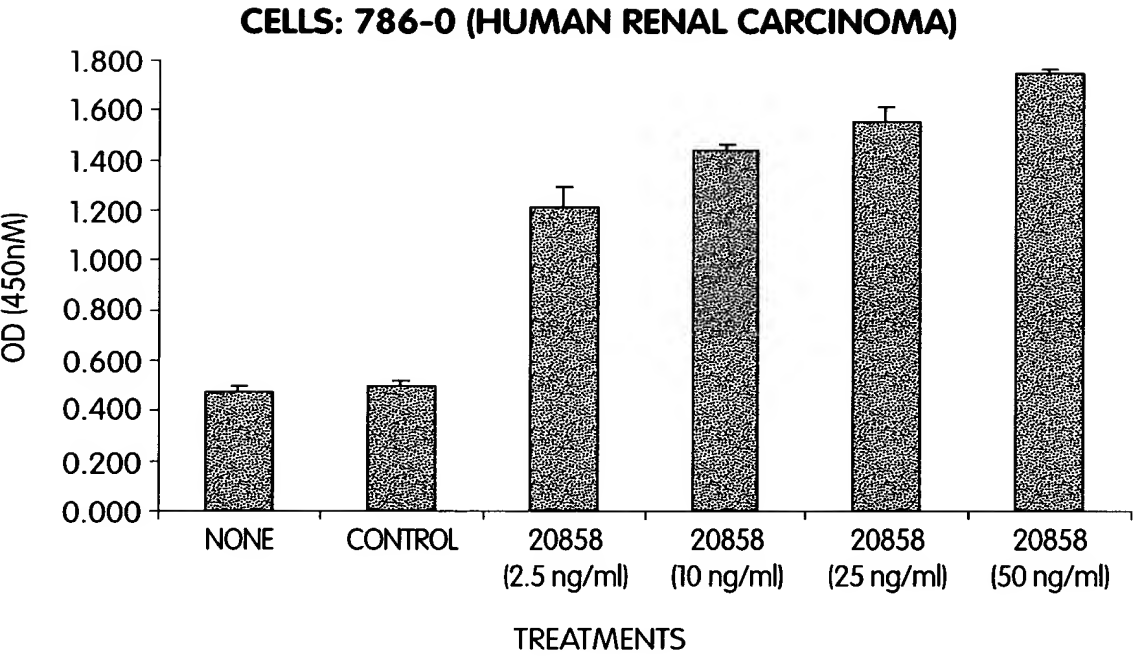


Fig. 22

RECEIVED
APR 24 2003
TECH CENTER 1000/2003



25/29

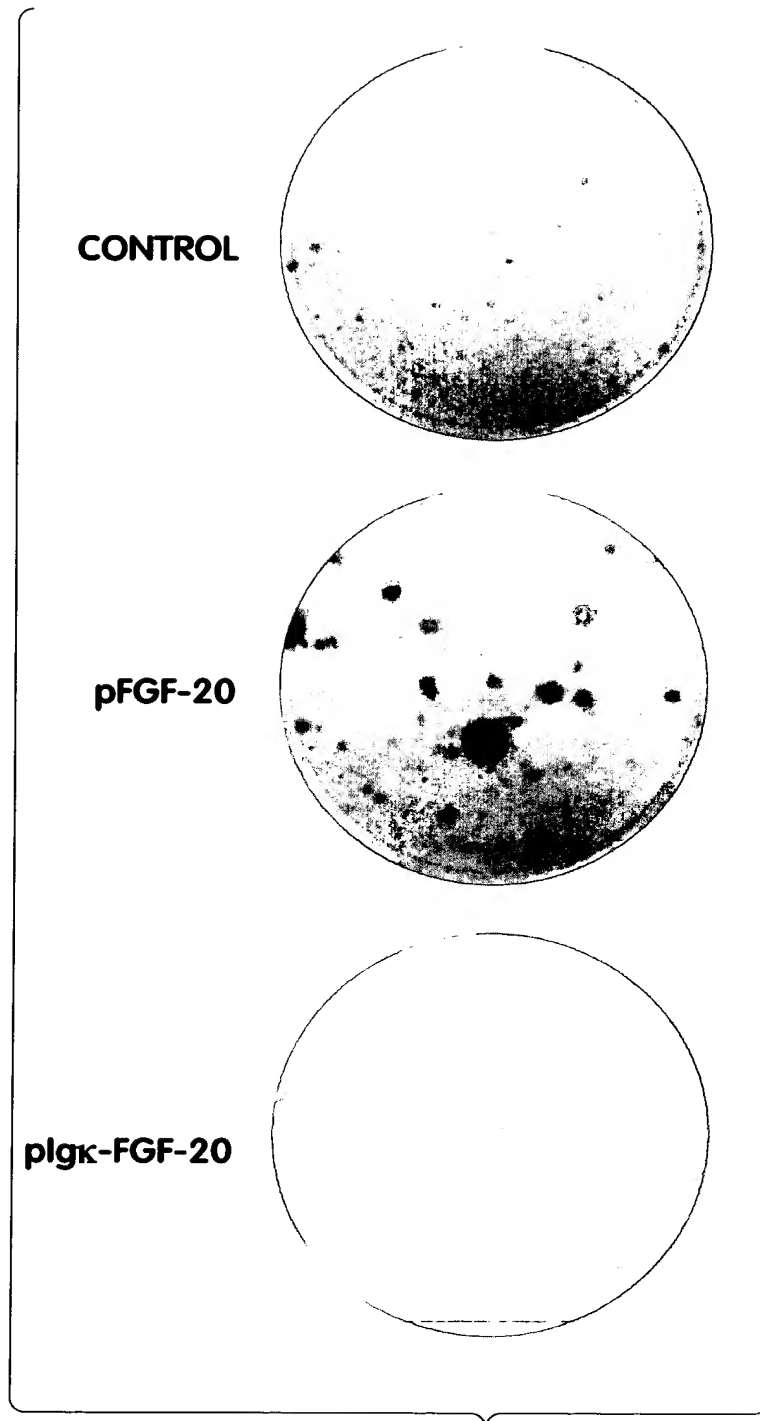


Fig. 23

RECEIVED
APR 24 2003
TECH CENTER 1600/2903



26/29

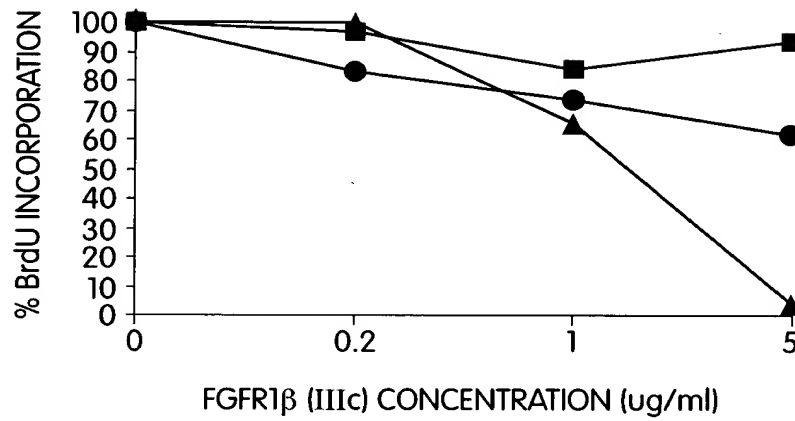


Fig. 24A

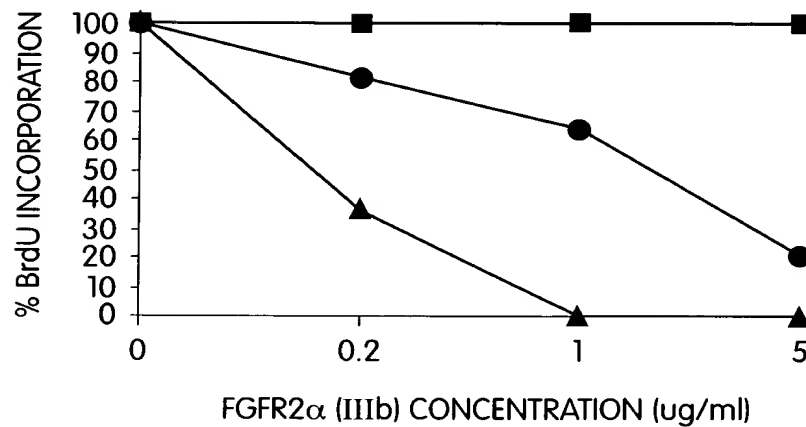


Fig. 24B

RECEIVED
APR 24 2003
TECH CENTER 1500/2900



27/29

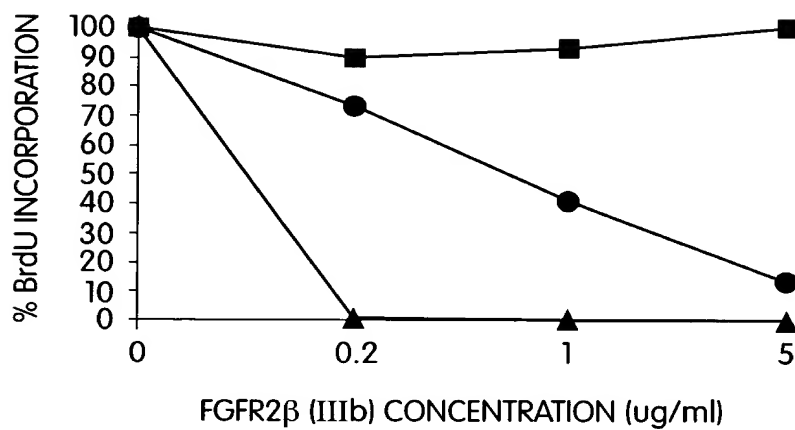


Fig. 24C

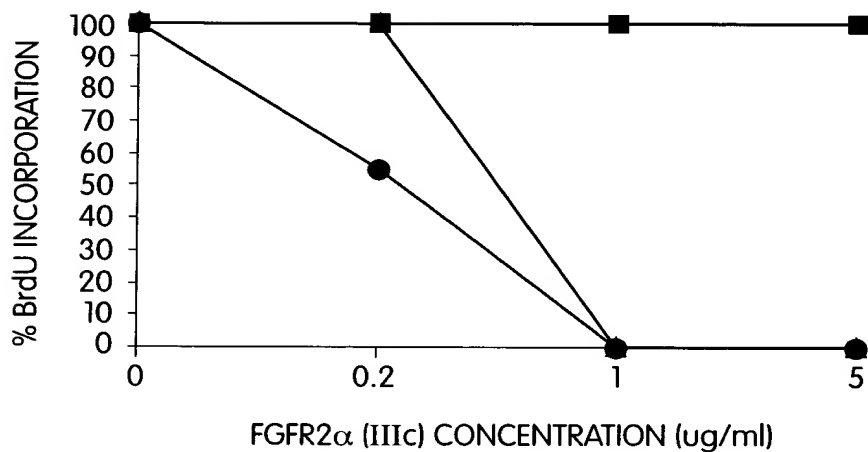


Fig. 24D

RECEIVED
APR 24 2003
TECH CENTER 1000/2900



28/29

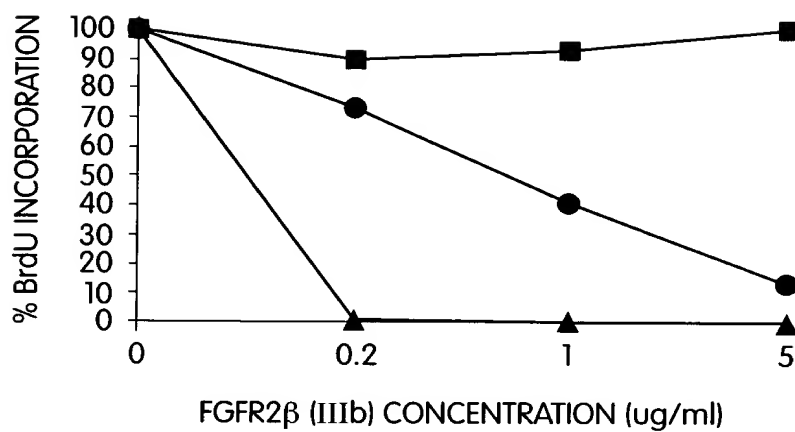


Fig. 24C

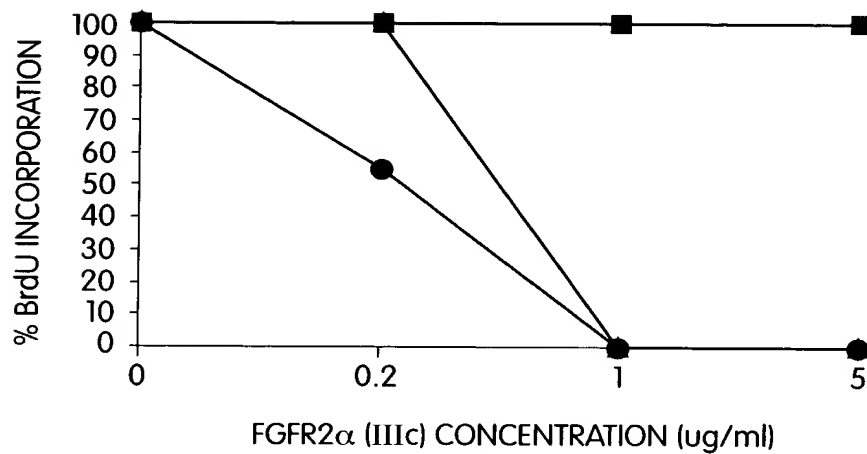


Fig. 24D

RECEIVED
APR 24 2003
TECH CENTER 1600/2900



29/29

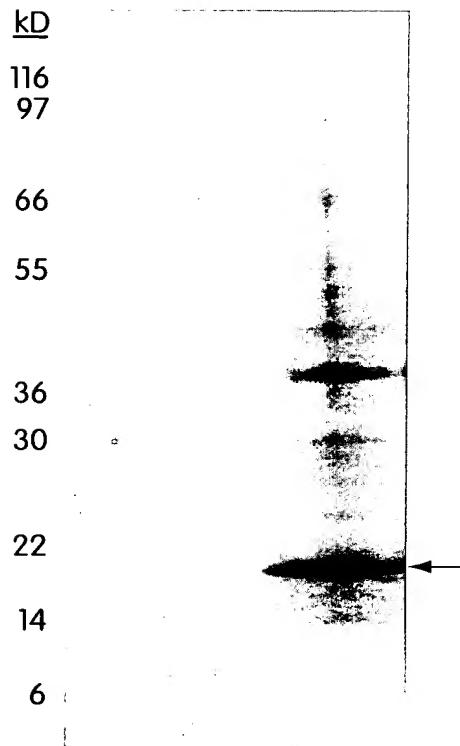


Fig. 25

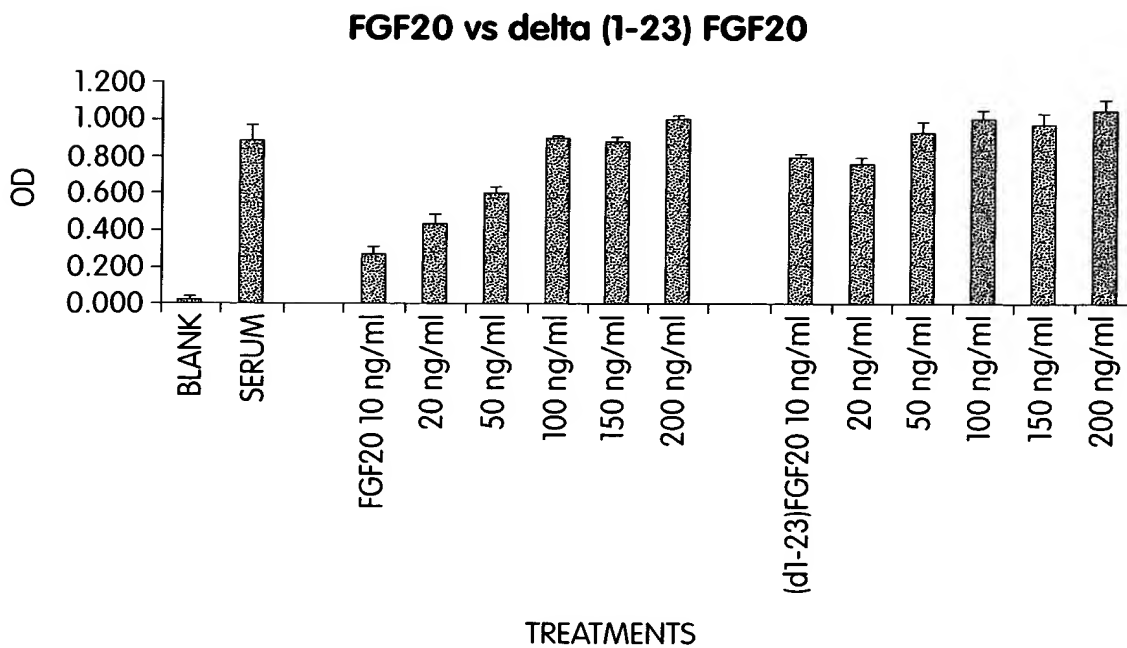


Fig. 26

RECEIVED
APR 24 2003
TECH CENTER 1600/2900